

Figure 1: Yeast Genome; One Mismatch; Truncation to length "L"
Theory and Measurements

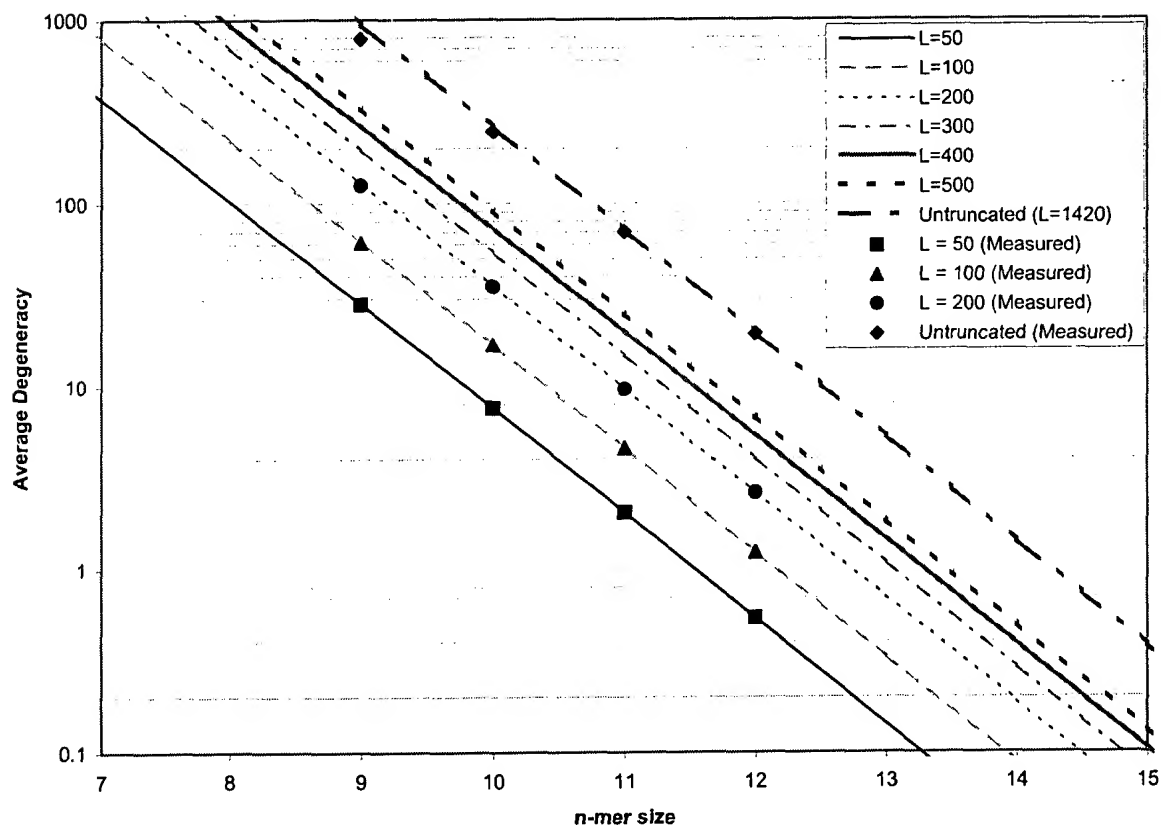


FIGURE 2

Figure 2: Mouse Genome; One Mismatch; Truncation to Length "L"
Theory and Measurements

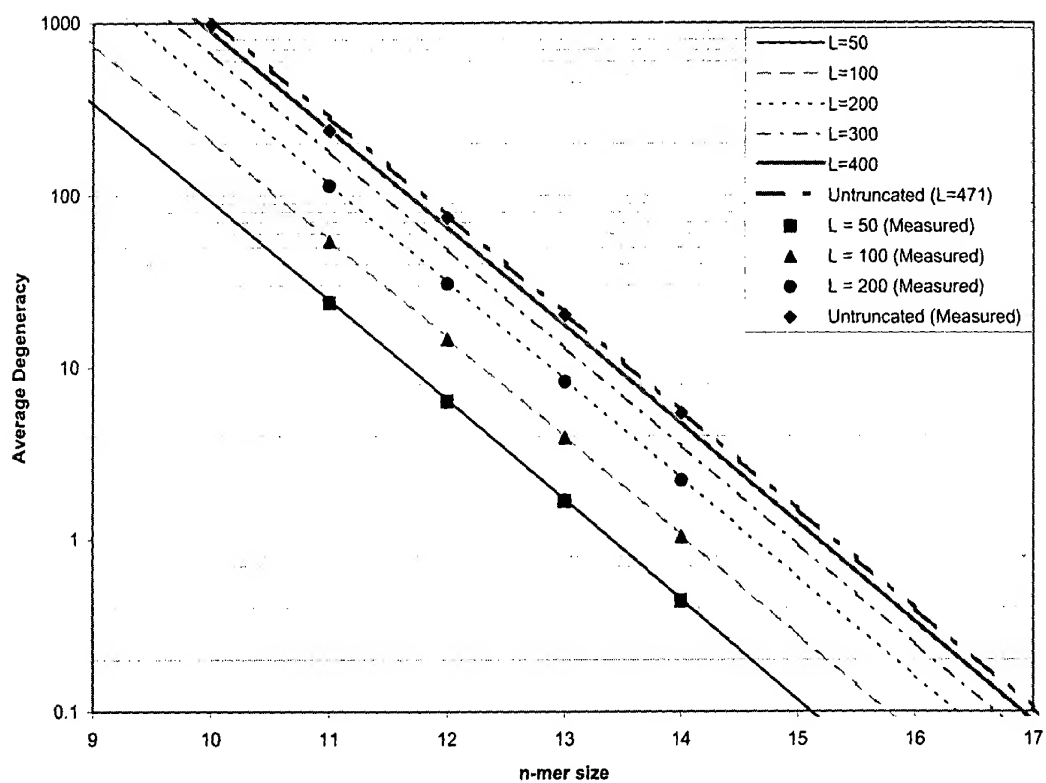


Figure 3: Relationships between parameter values such that average degeneracy = 1 (theoretical predictions)

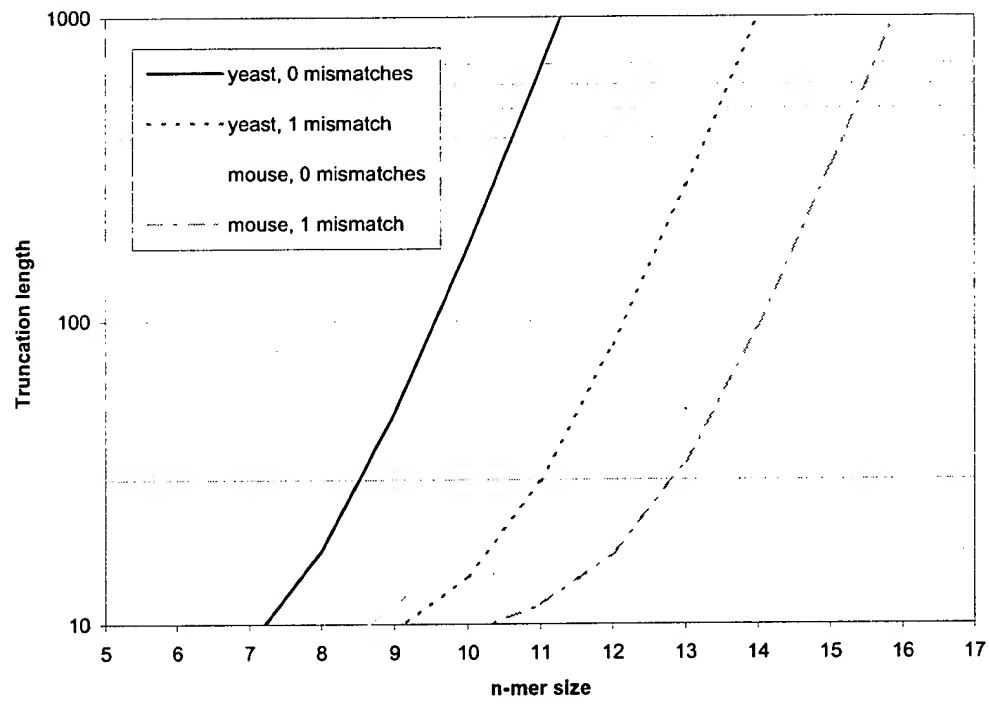


FIG. 4A

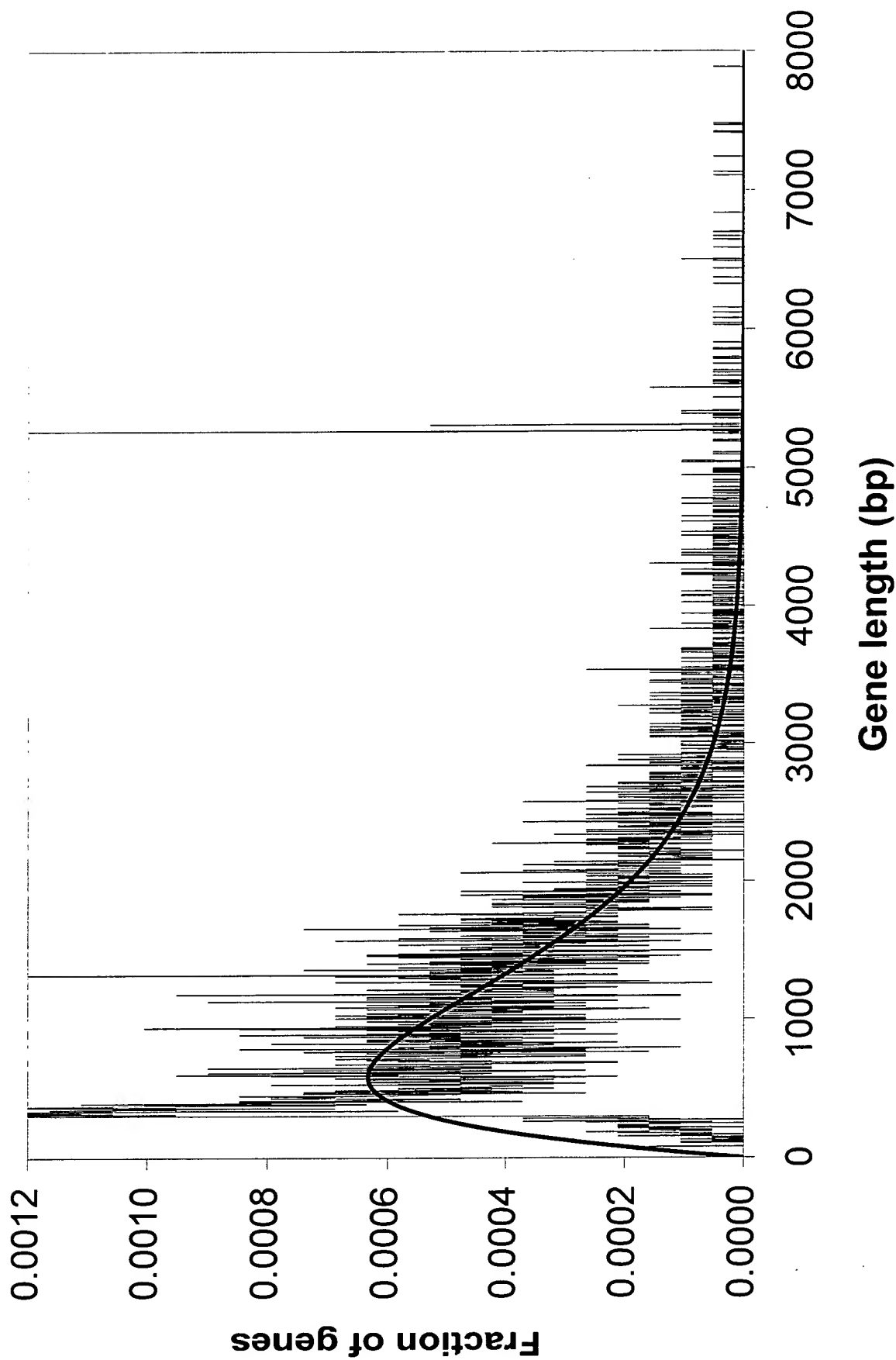


FIG. 4B

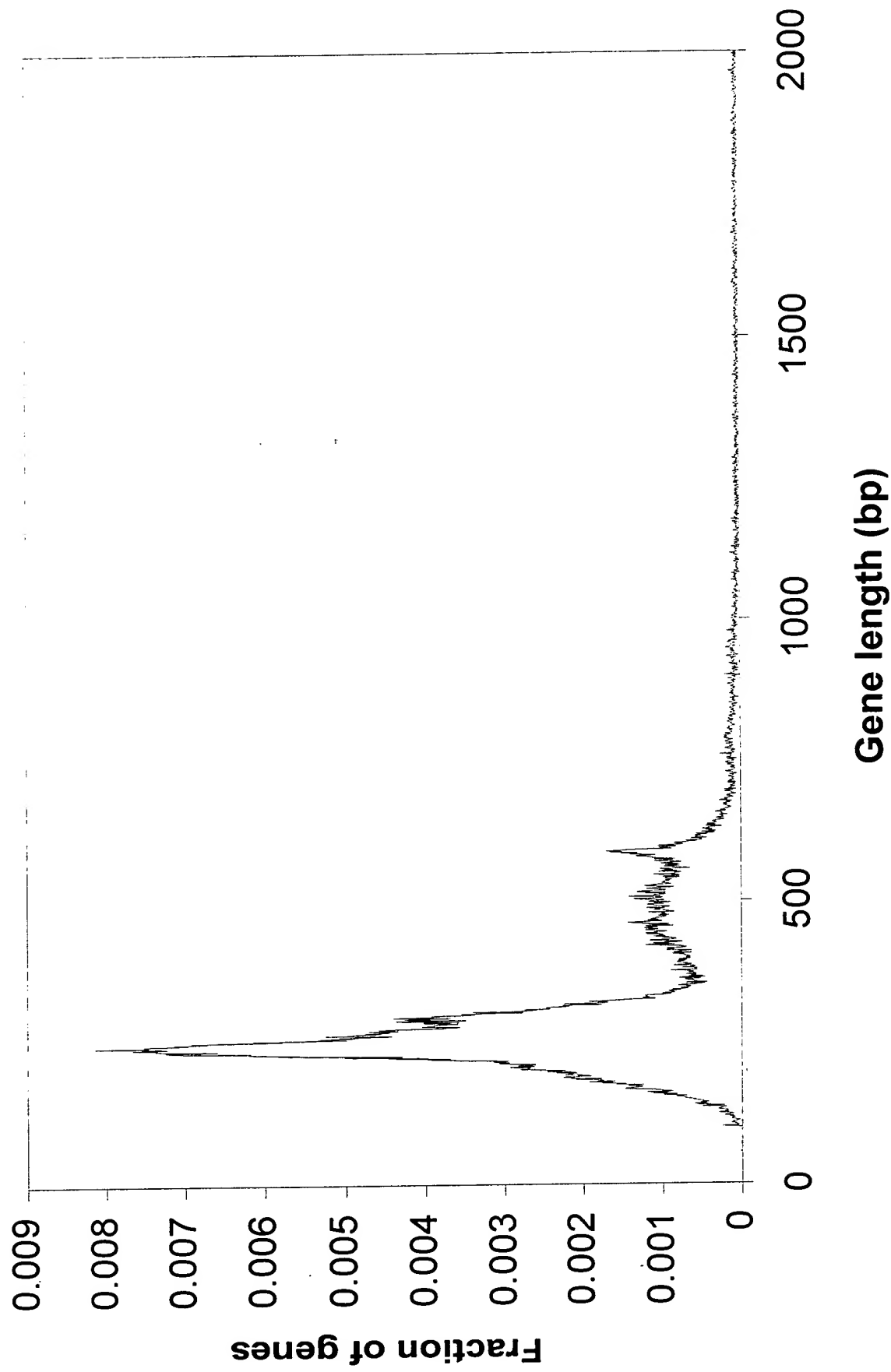


FIG. 5A

8-mers; mismatches: 0

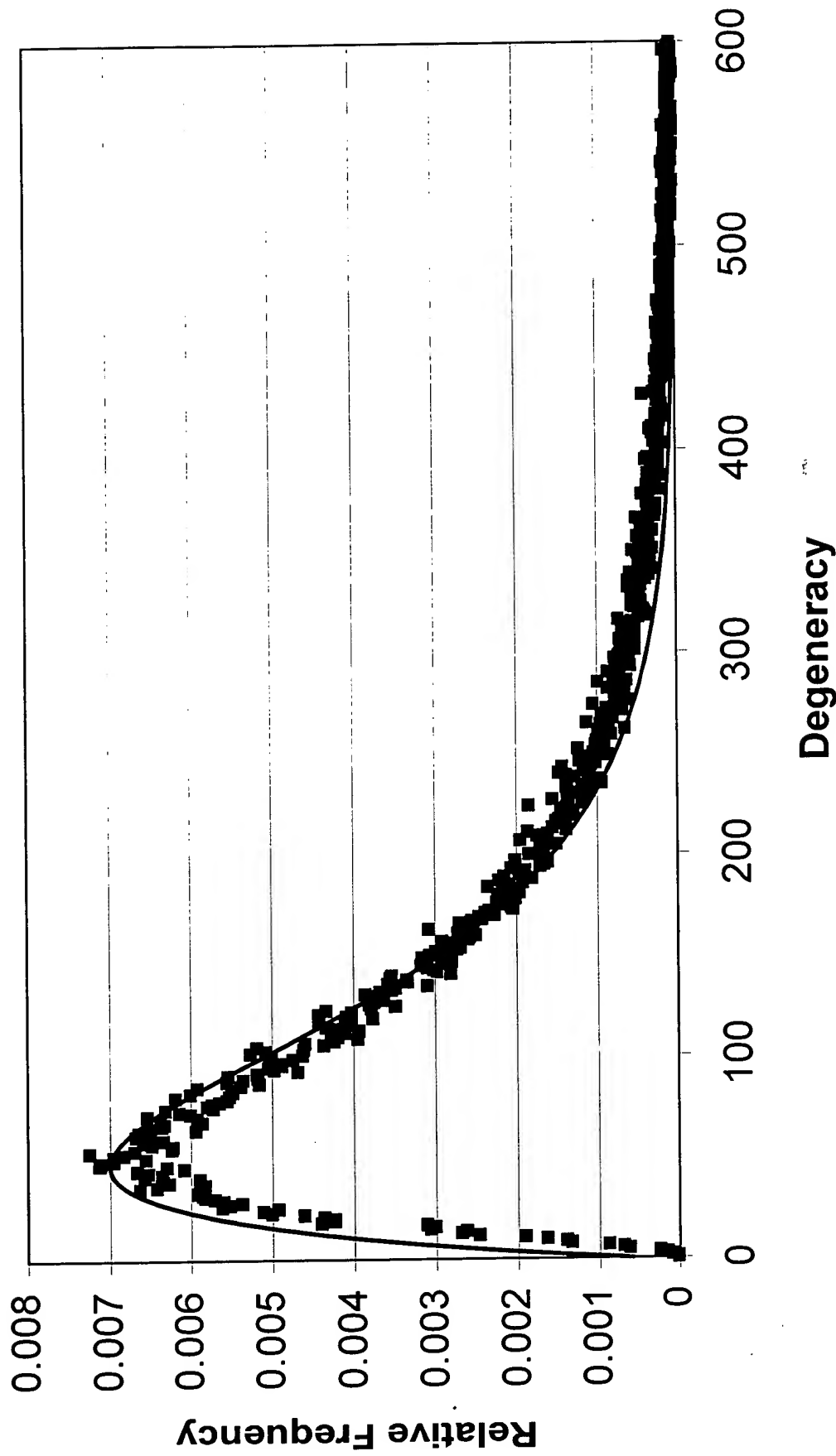


FIG 5B

8-mers; mismatches: 1

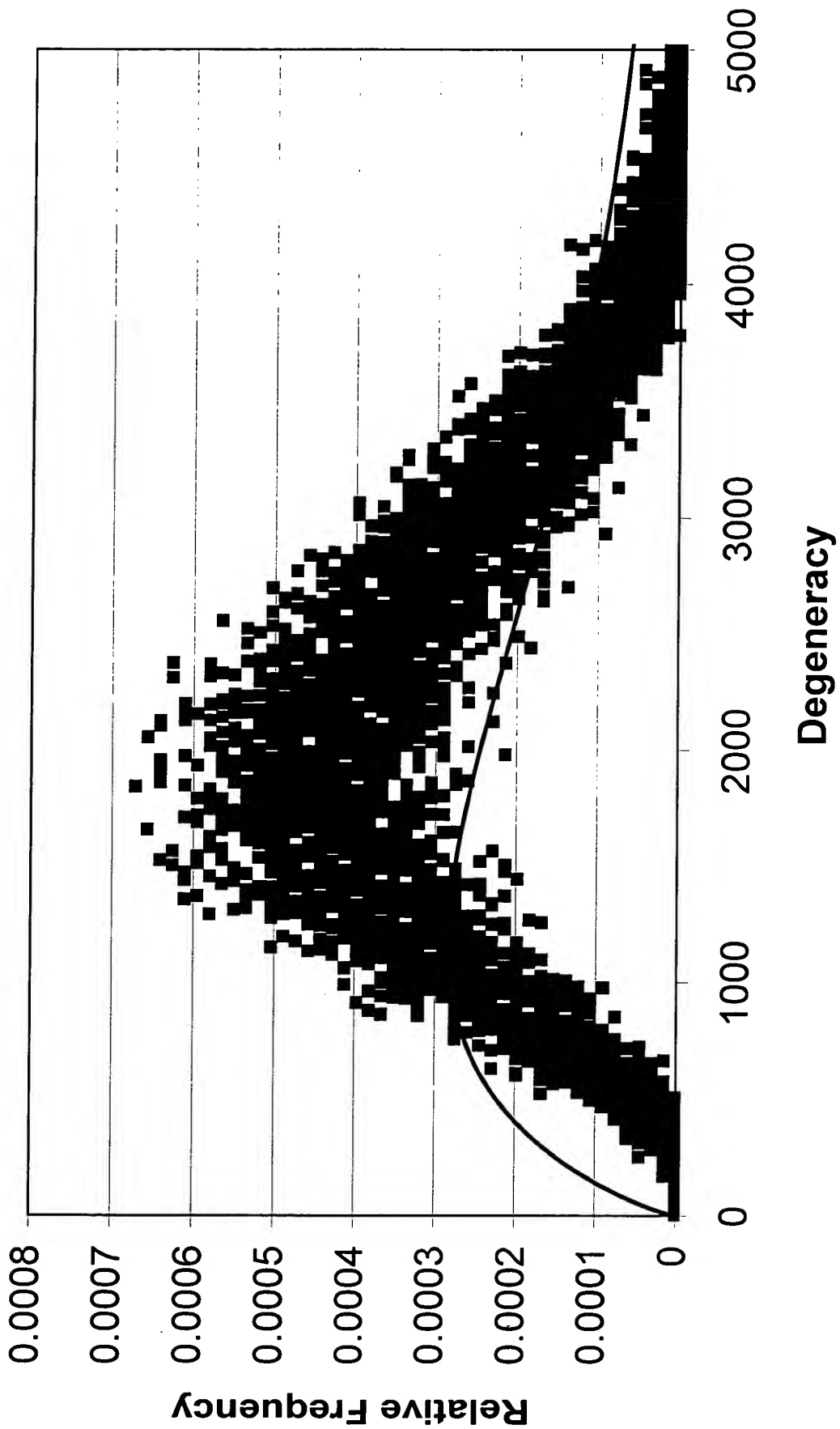


TABLE 3.4.3.3.3

FIG. 5C

9-mers; mismatches: 0

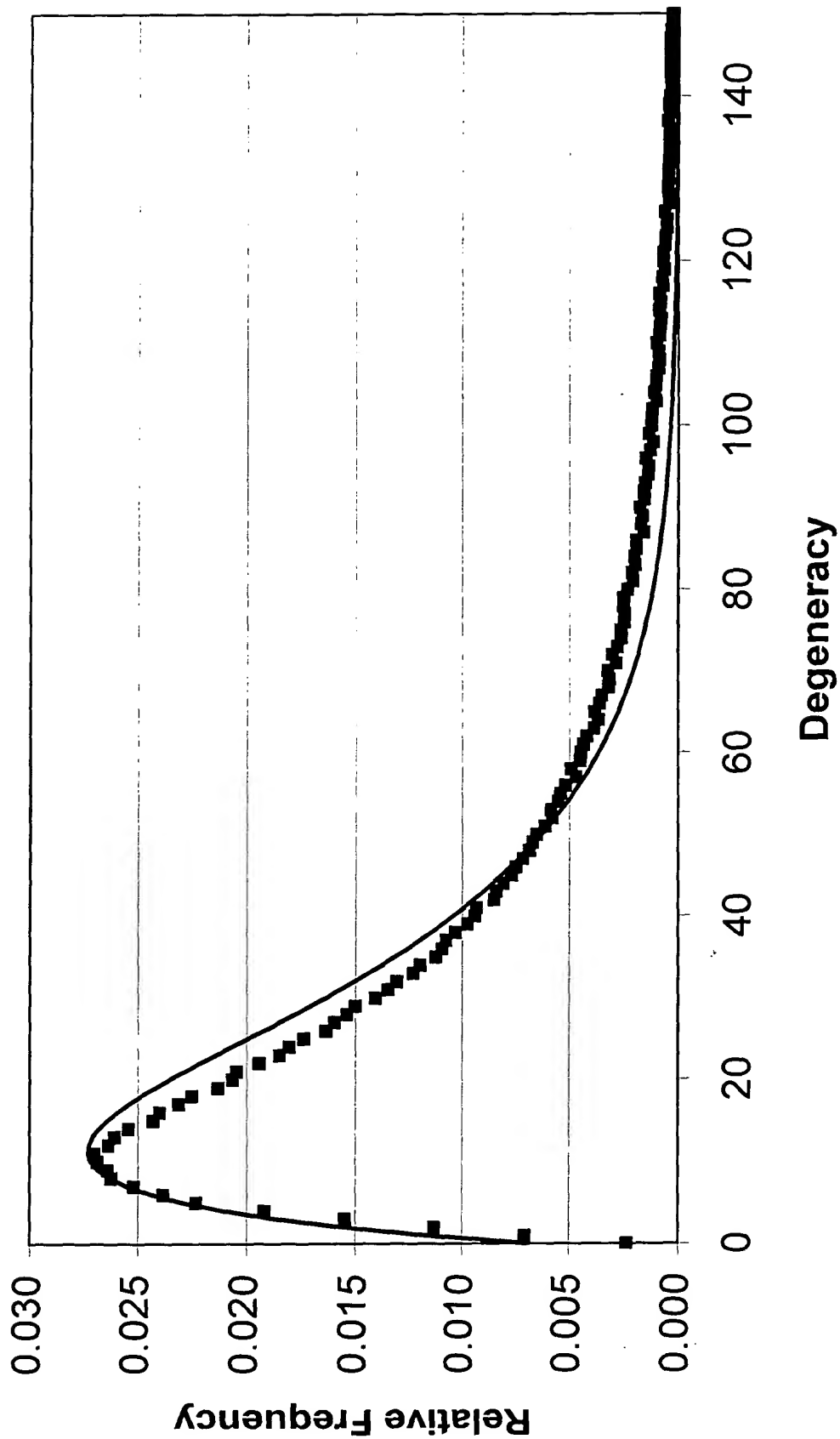


FIG. 5D

9-mers; mismatches: 1

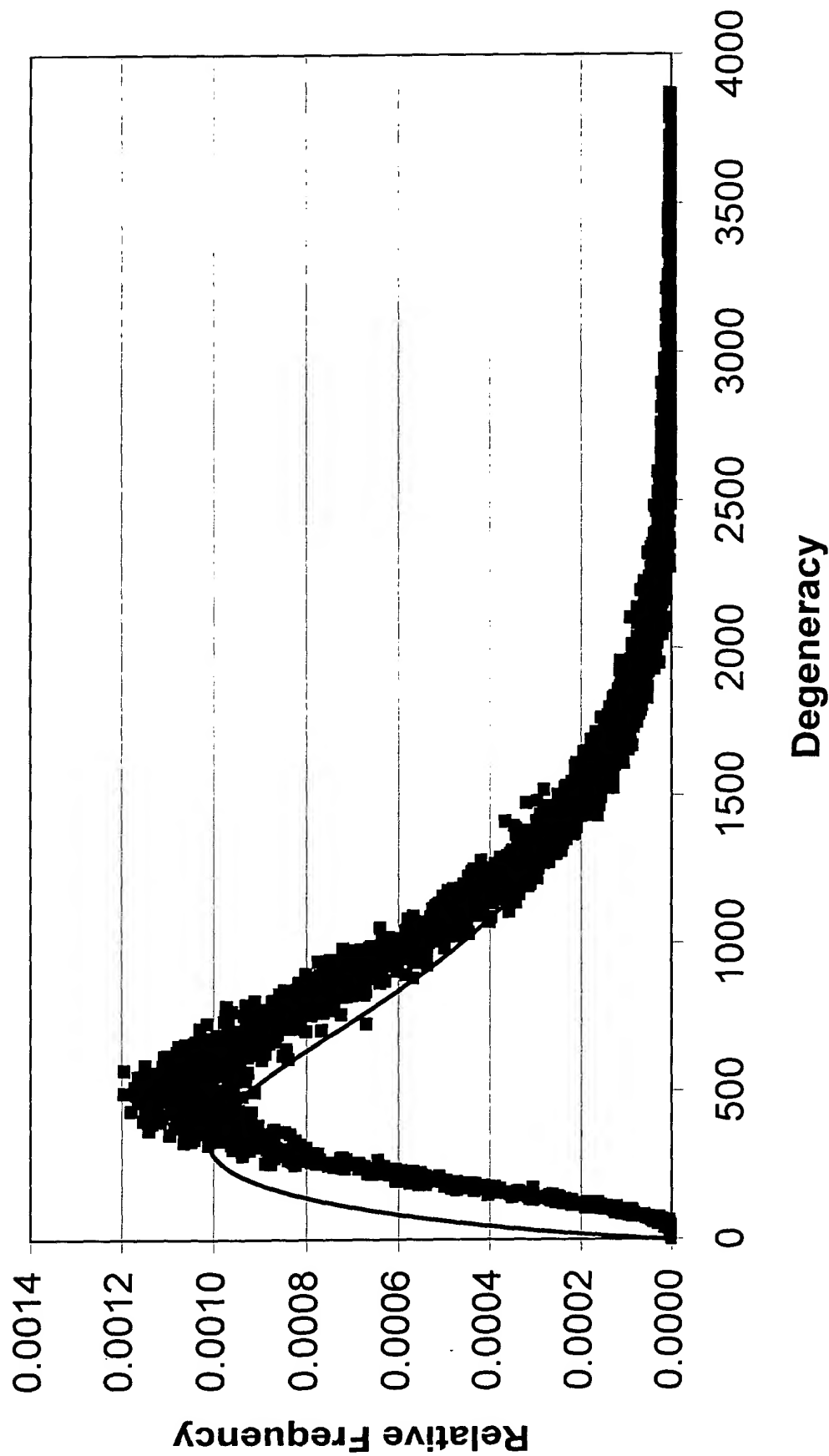
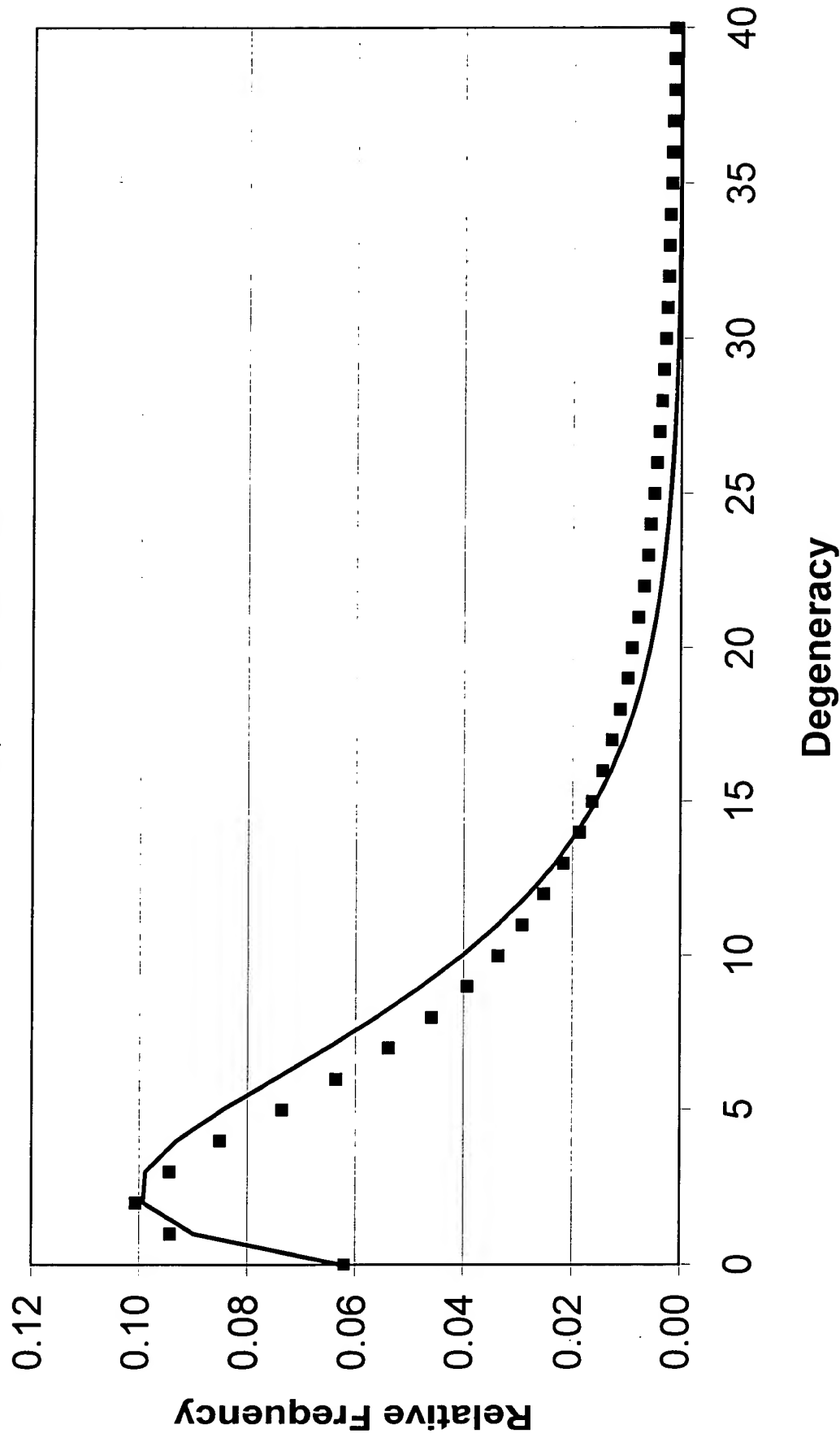


FIG 5E

10-mers; mismatches: 0



10-mers; mismatches: 1

FIG. 5F

10-mers; mismatches: 1

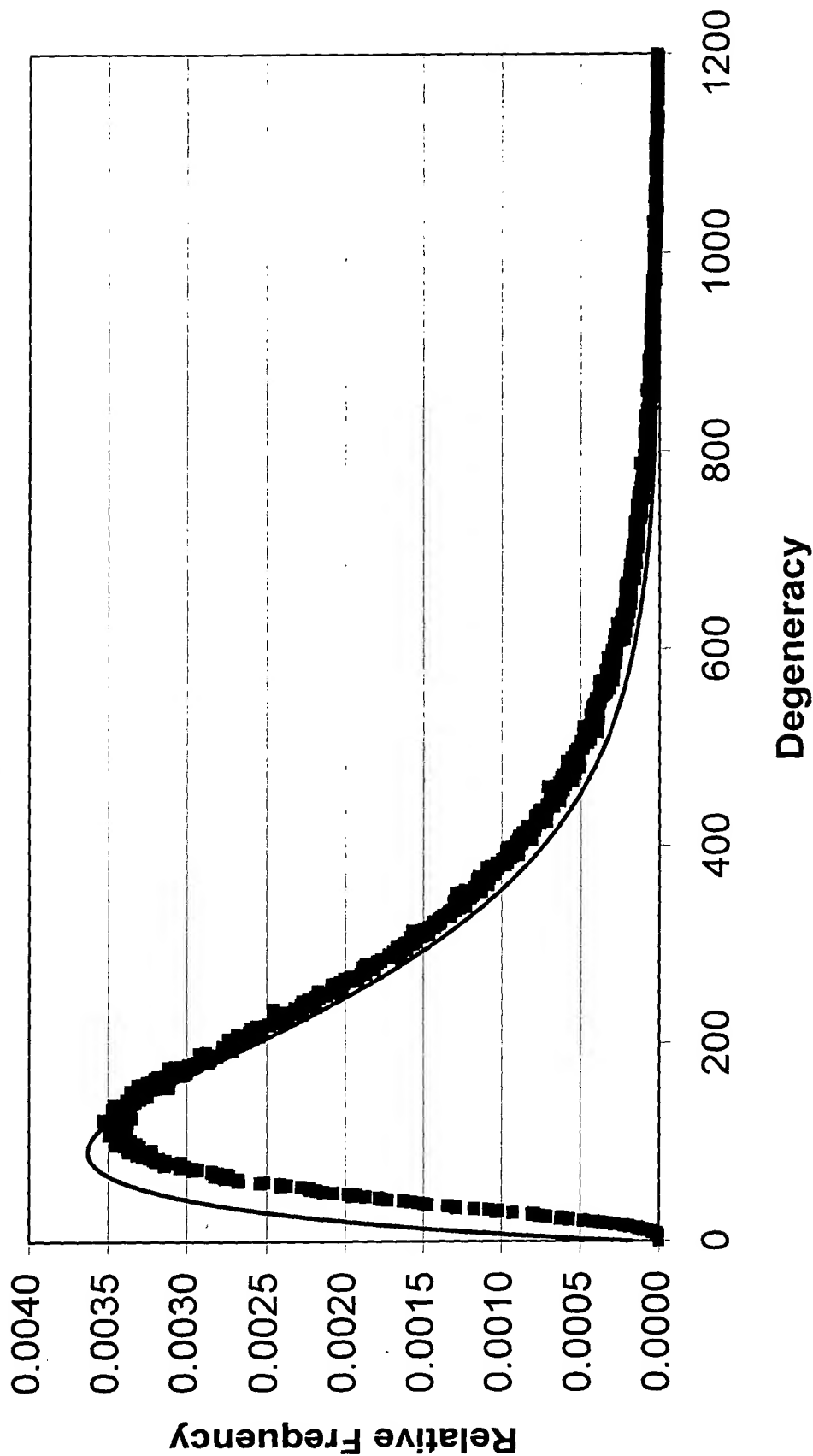


FIG. 5G

11-mers; mismatches: 0

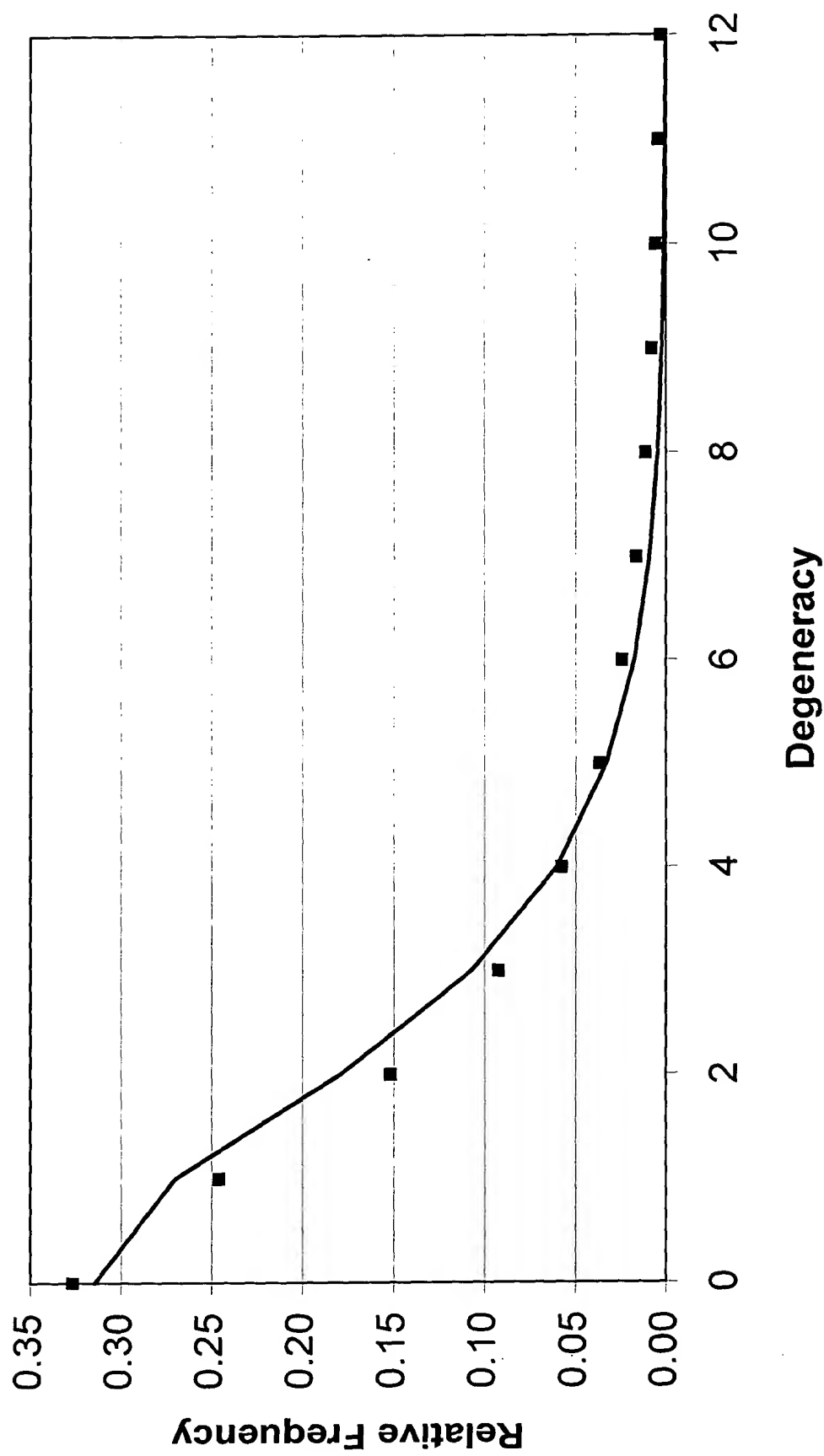
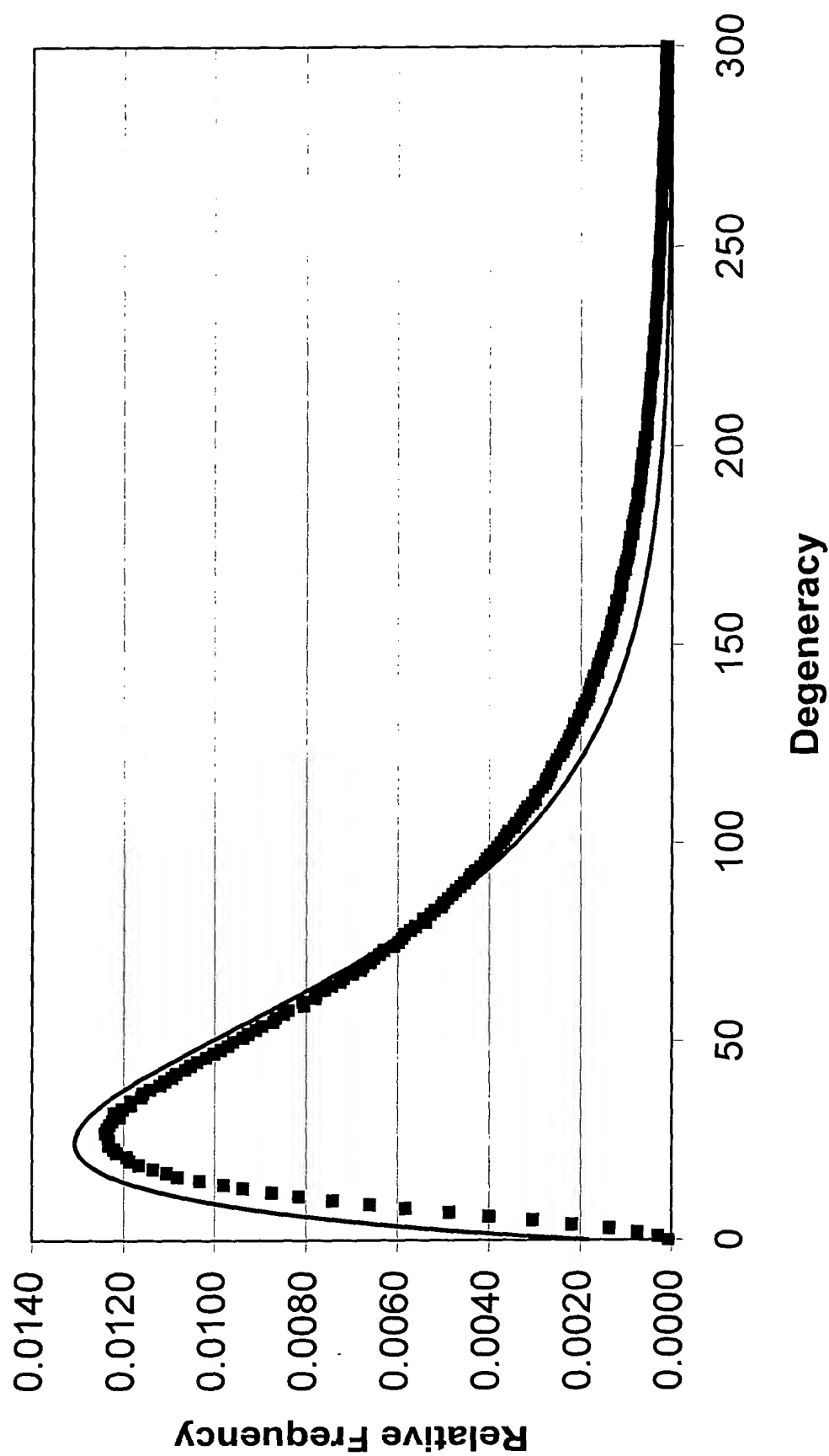


FIG. 5H

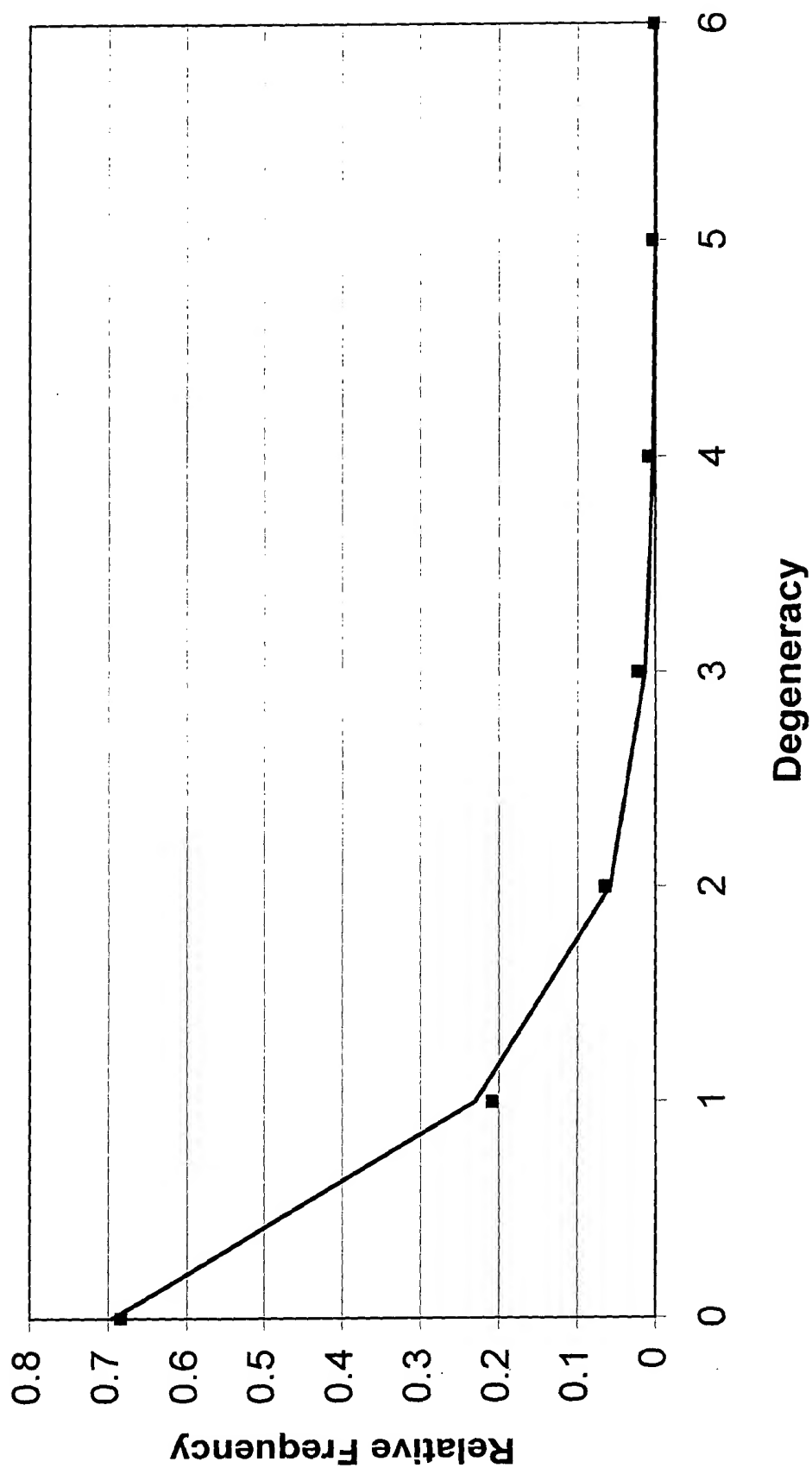
11-mers; mismatches: 1



FOR CHANGES

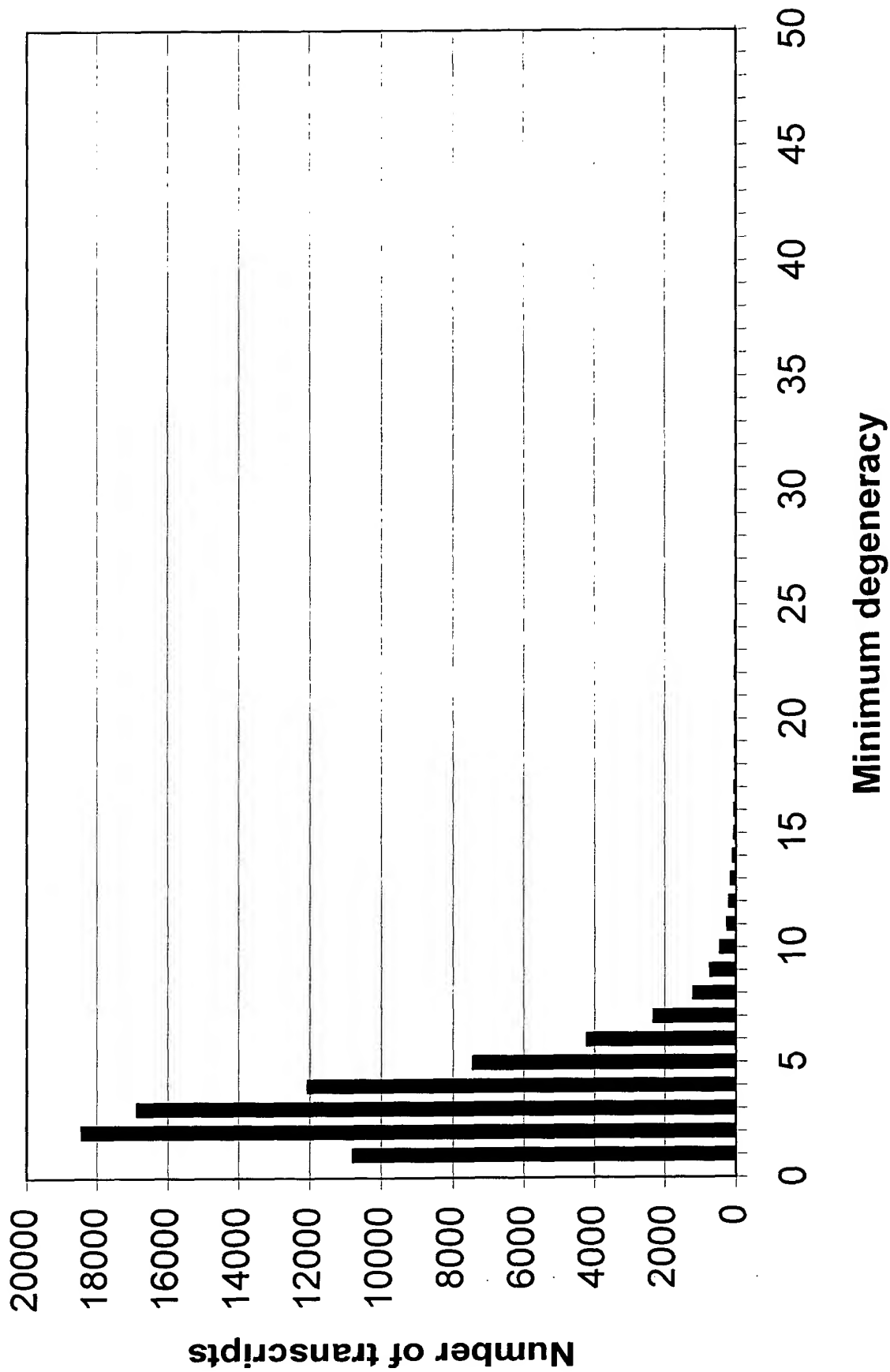
FIG. 5I

12-mers; mismatches: 0



TOP SECRET

FIG. 6A



TC5000-00000000

FIG. 4B

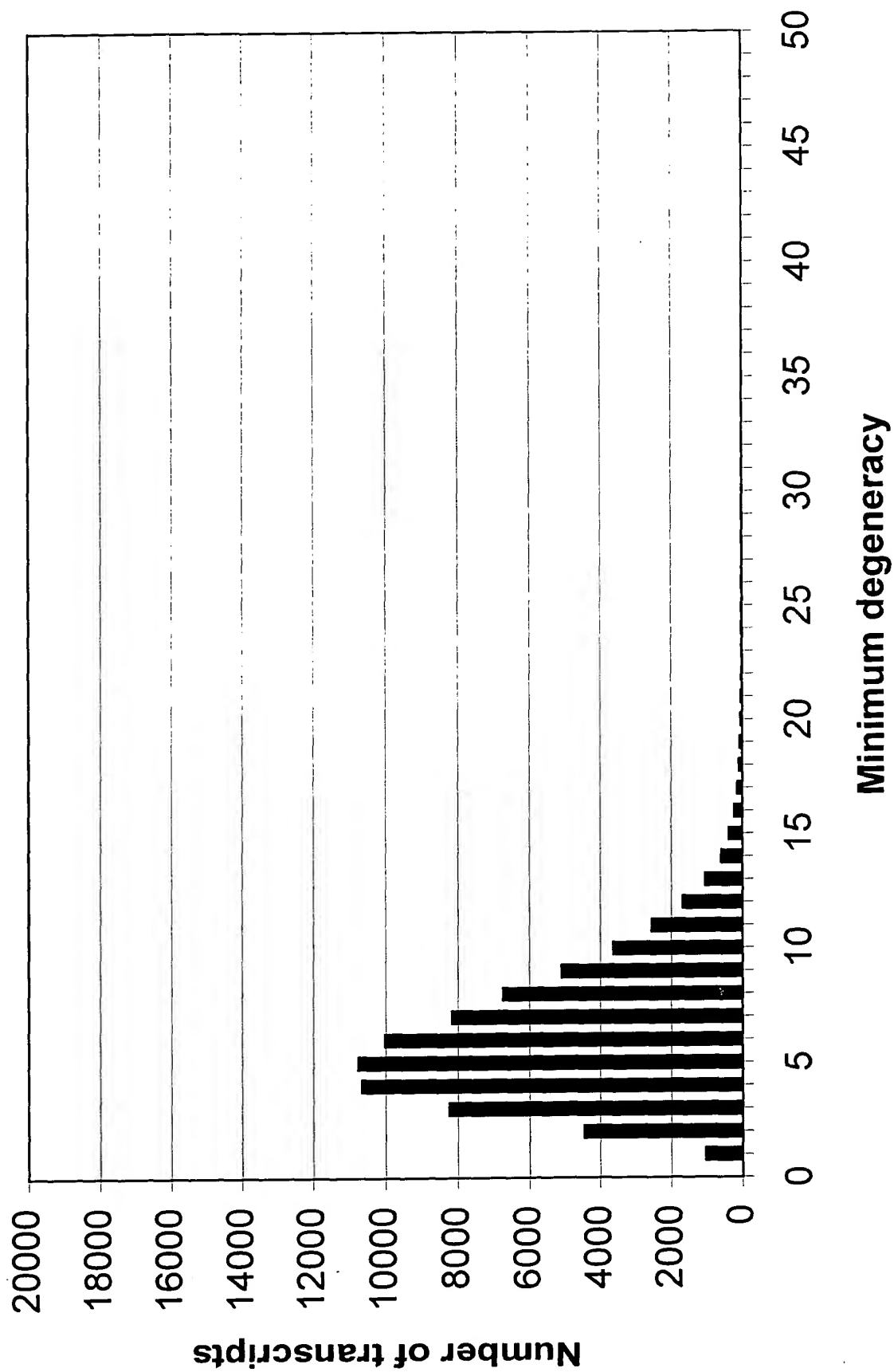


TABLE 5

FIG. 6C

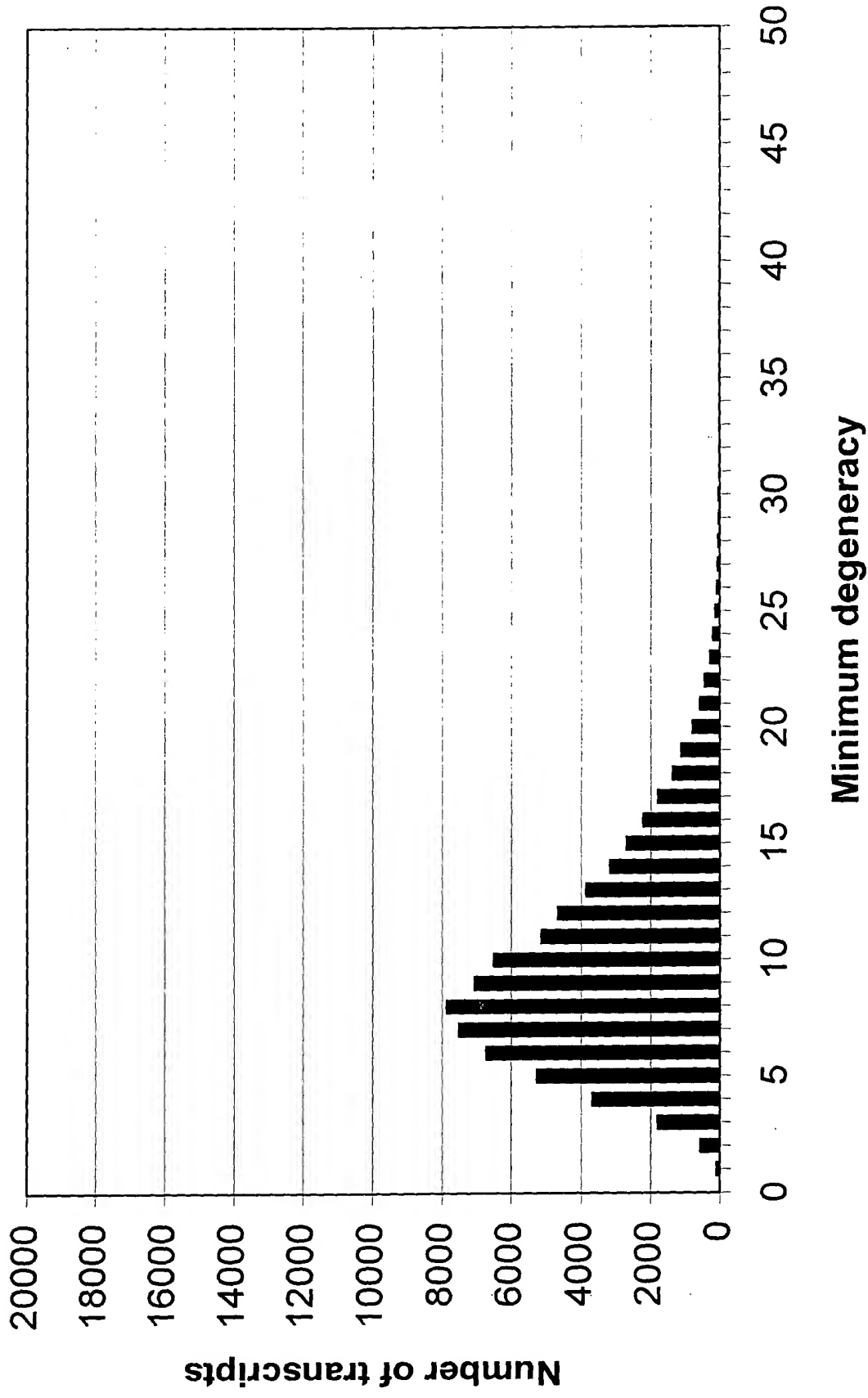


FIGURE 4D

FIG. 4D

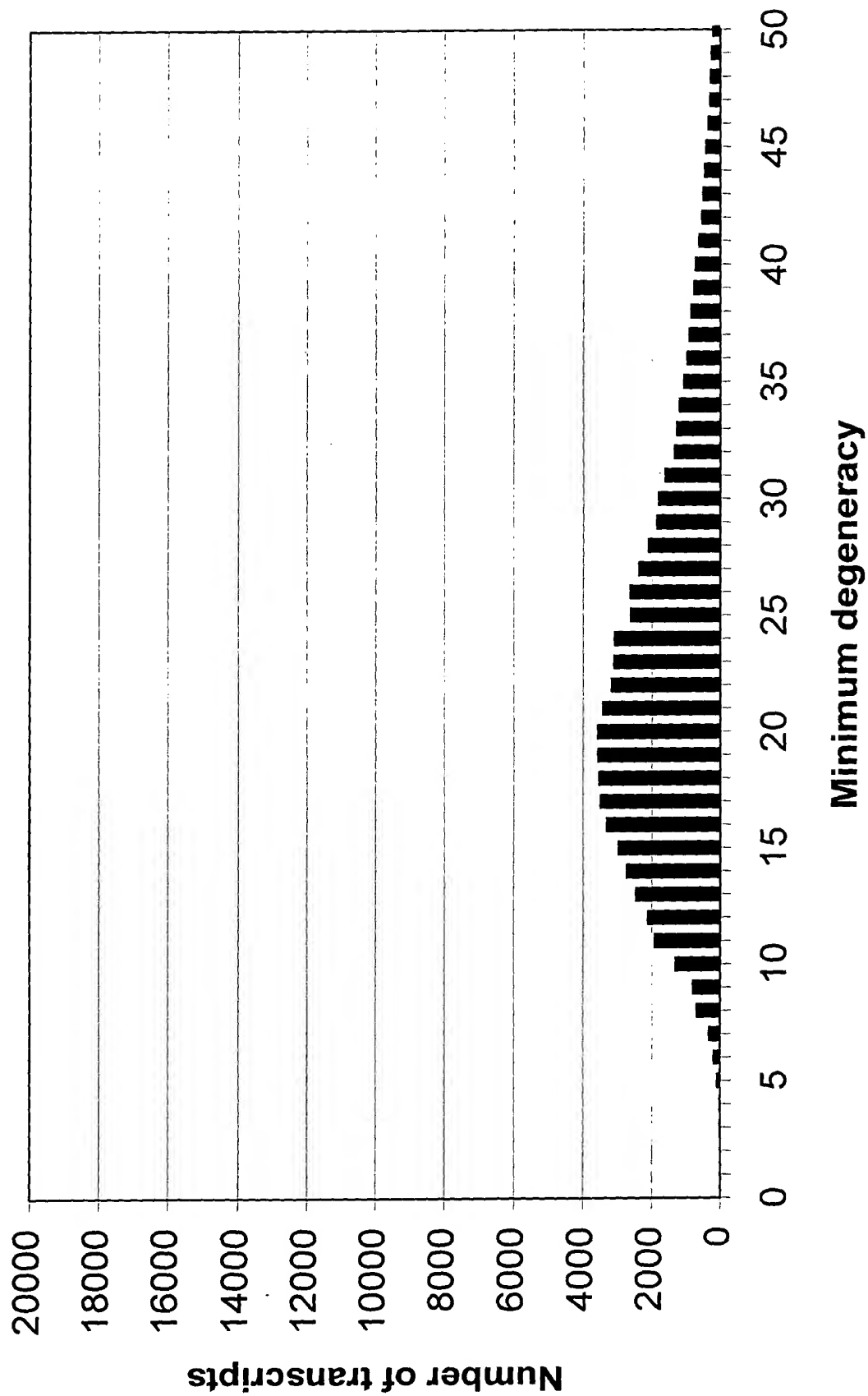
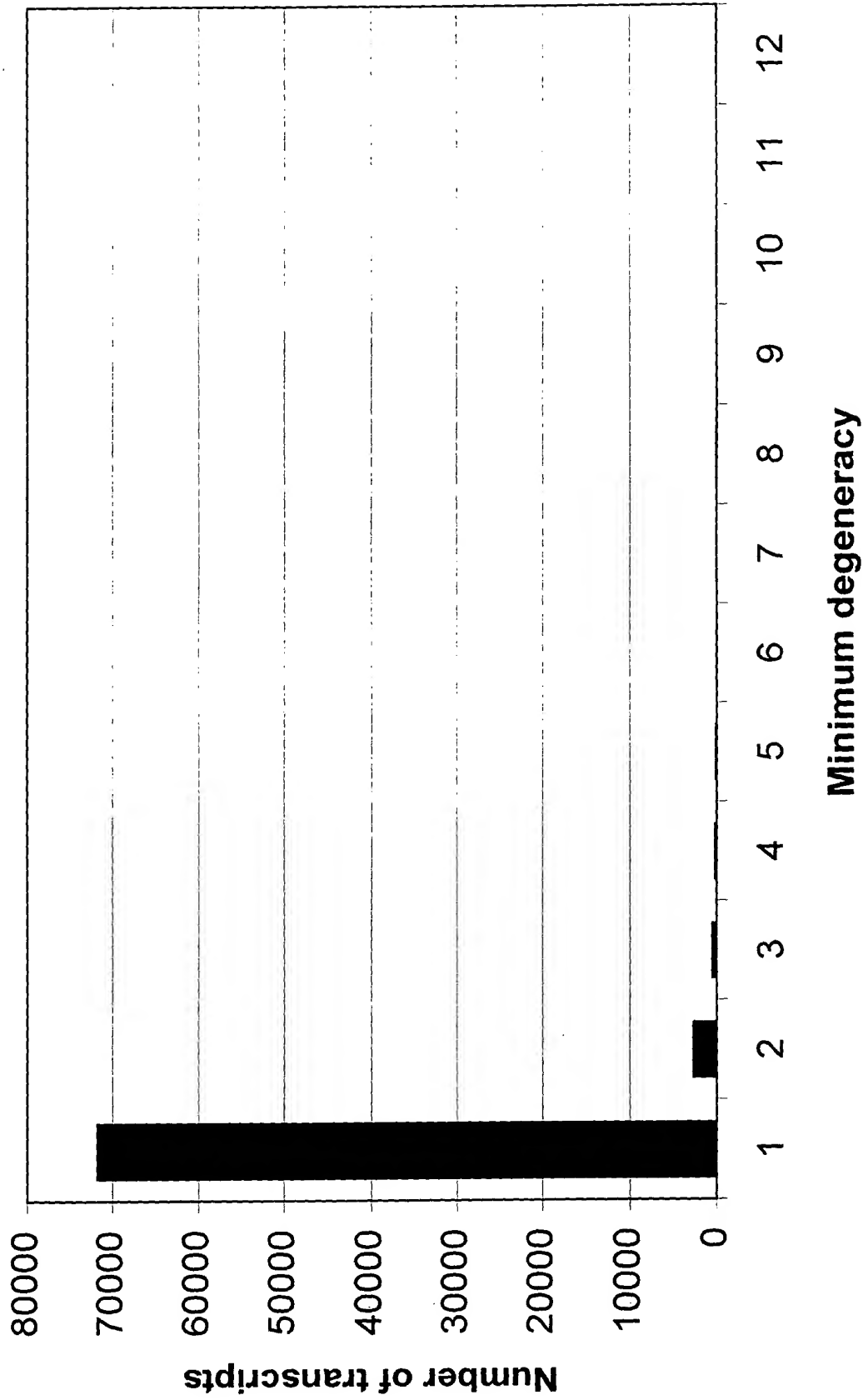


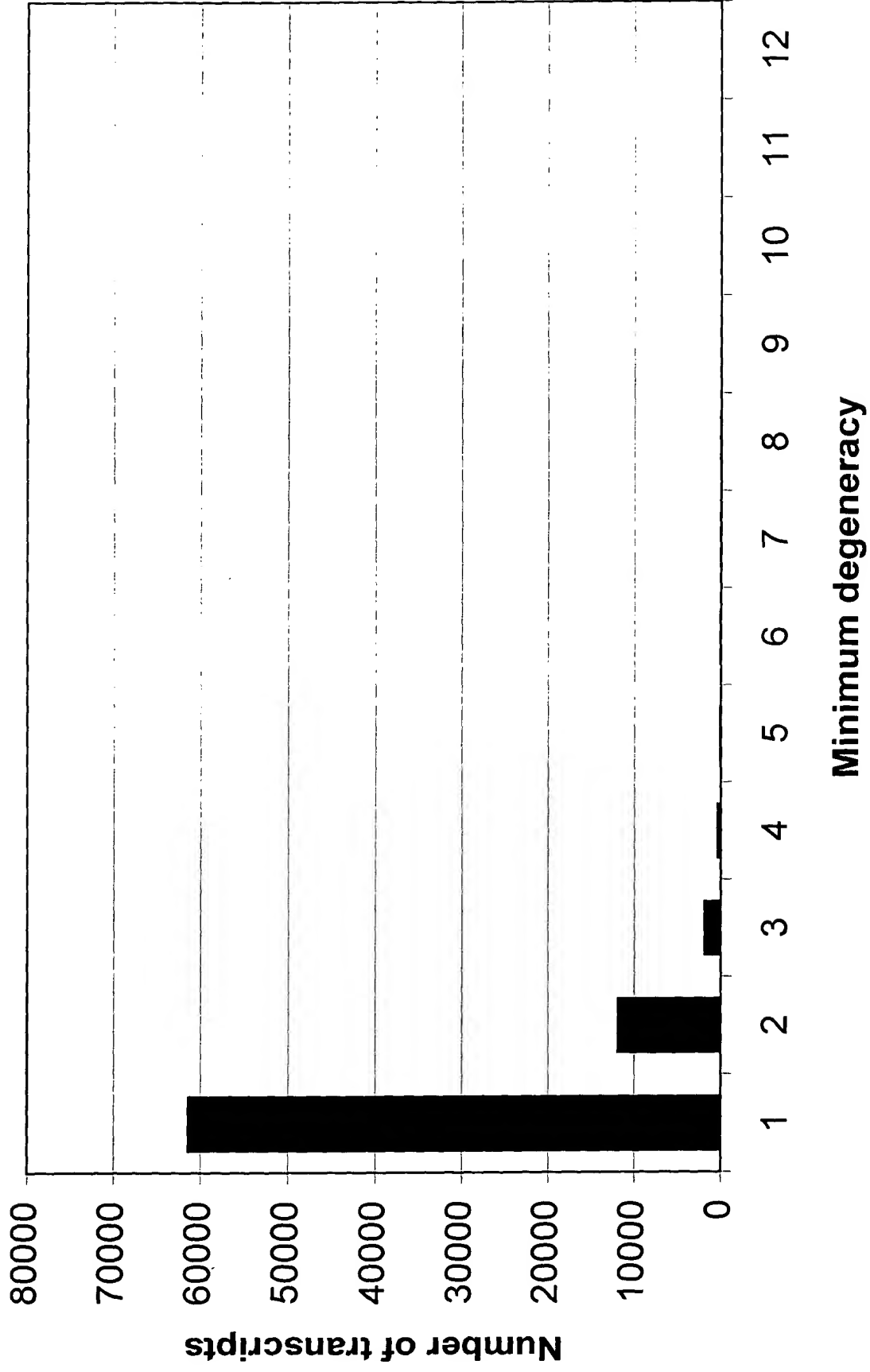
Figure 1

FIG. 1

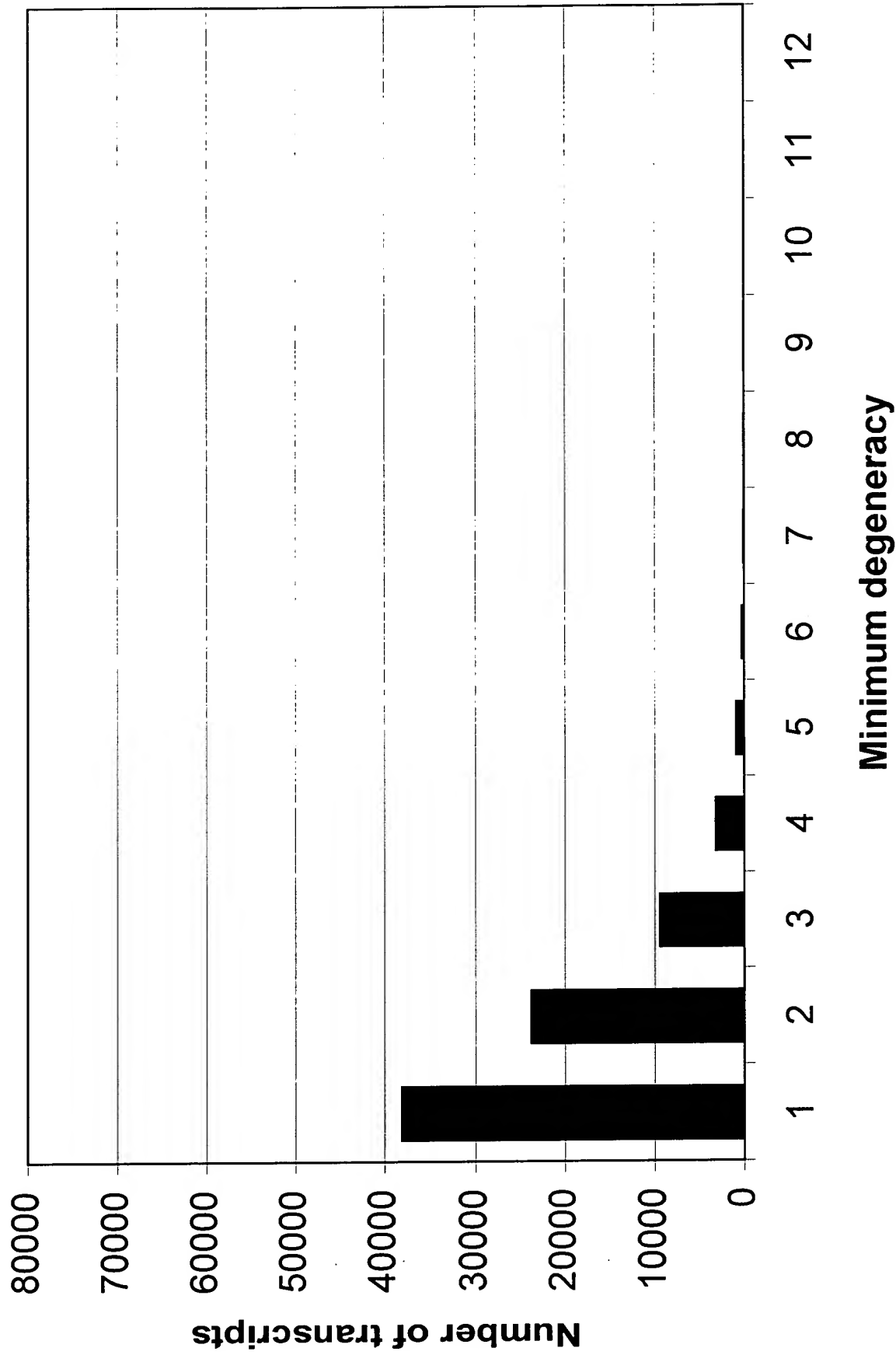


FOR SEVERAL

FIG. 6F



total 340000
FIG. 6G



FOREFEET SETH00880

FIG. 6H

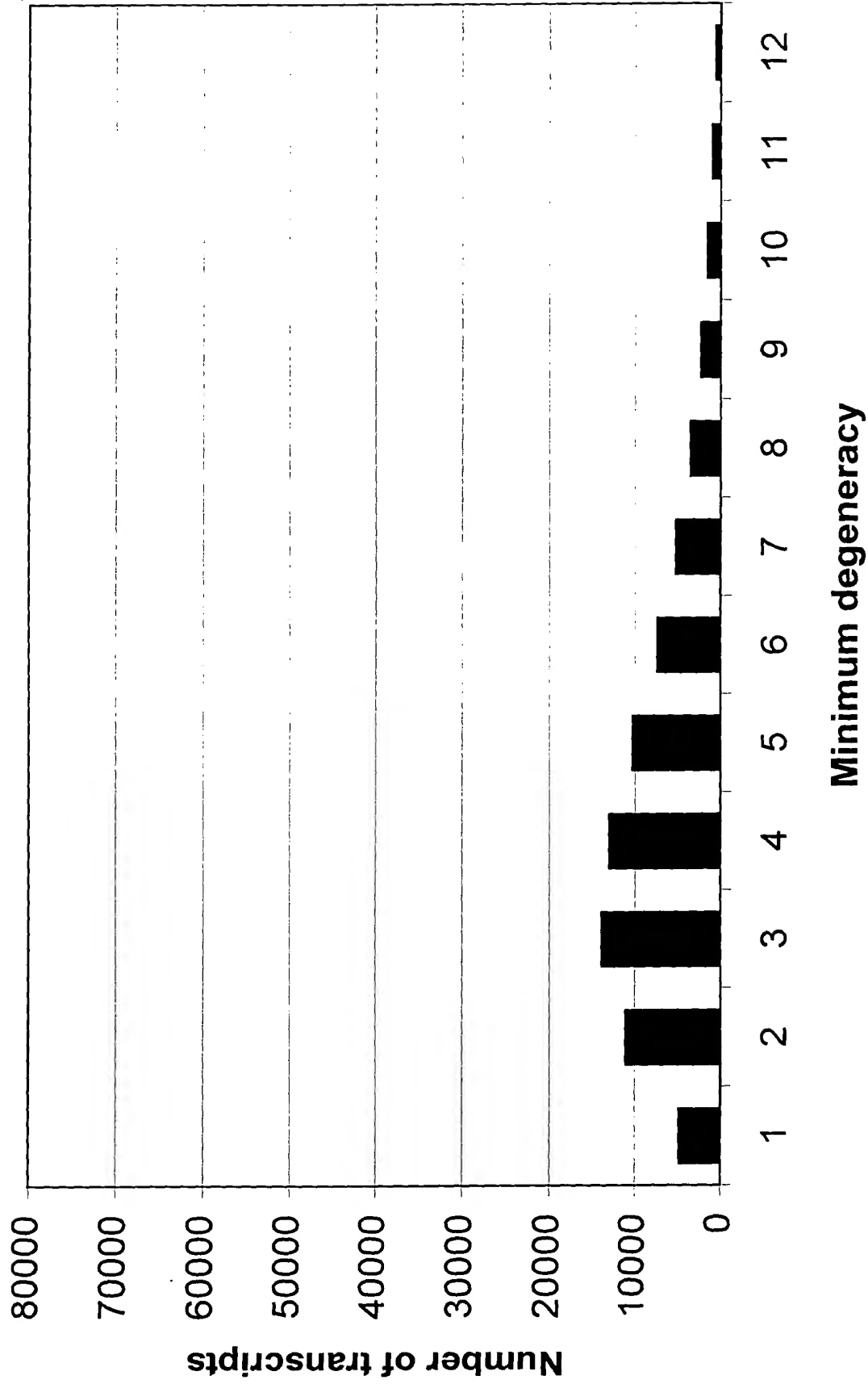


FIG. 7A

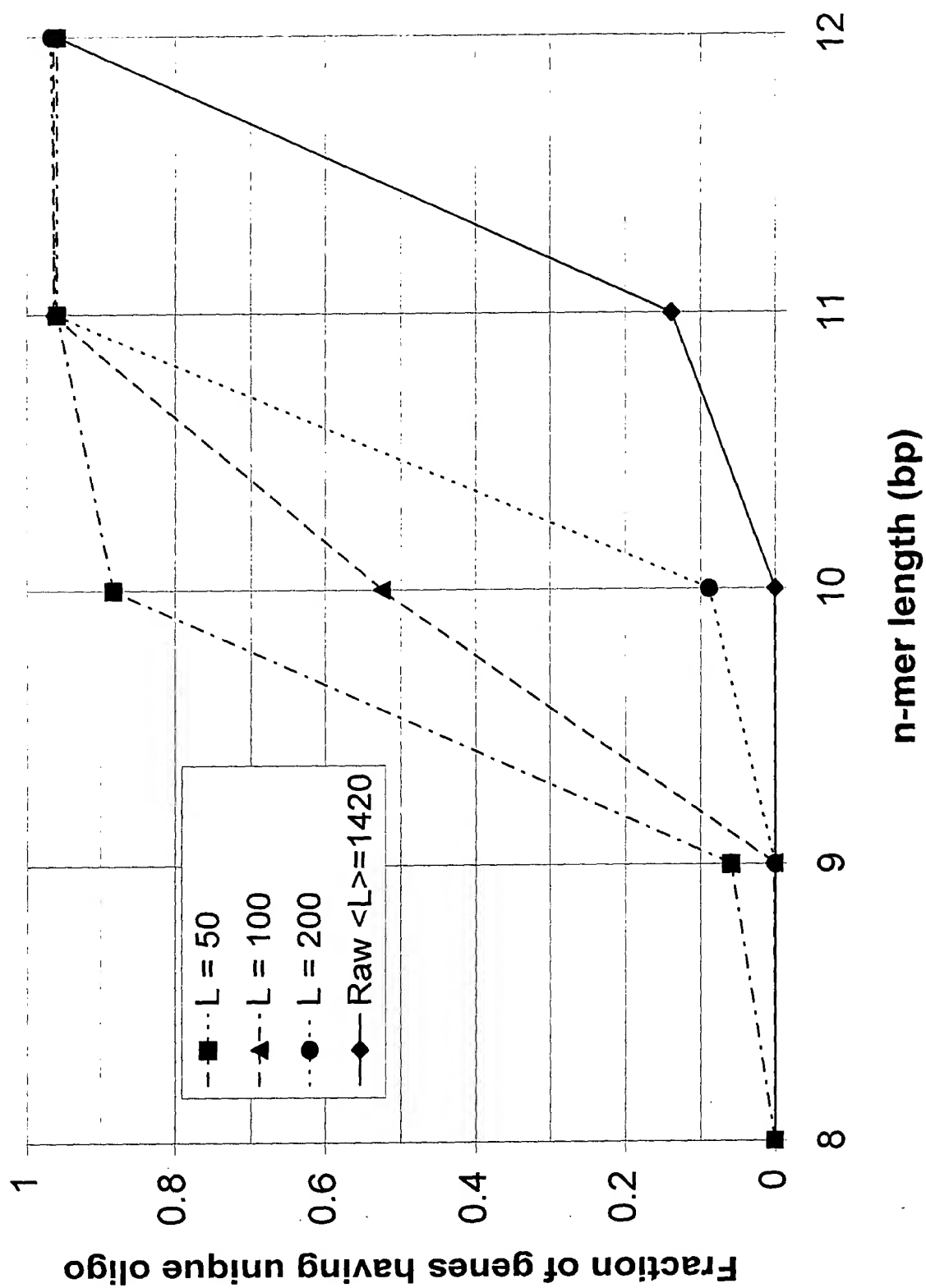


FIG. 7B

